

OIIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/967,107

DATE: 11/06/2001
 TIME: 09:43:10

Input Set : A:\PTO_VSK.txt
 Output Set: N:\CRF3\11062001\I967107.raw

**Does Not Comply
 Corrected Diskette Needed**

5 <110> APPLICANT: PFIZER INC.
 7 THOMPSON, JOHN F.
 11 <120> TITLE OF INVENTION: ASSAY FOR THE DETERMINATION OF FUNCTIONAL BINDING OF
 COMPOUNDS TO
 12 RECEPTORS
 16 <130> FILE REFERENCE: PC10217AJAK
 C--> 20 <140> CURRENT APPLICATION NUMBER: US/09/967,107
 C--> 20 <141> CURRENT FILING DATE: 2001-09-28
 20 <150> PRIOR APPLICATION NUMBER: US 60/237,544
 22 <151> PRIOR FILING DATE: 2000-09-30
 26 <160> NUMBER OF SEQ ID NOS: 6
 30 <170> SOFTWARE: PatentIn version 3.1
 34 <210> SEQ ID NO: 1
 36 <211> LENGTH: 29
 38 <212> TYPE: DNA
 C--> 40 <213> ORGANISM: Artificial
 W--> 44 <220> FEATURE:
 W--> 44 <223> OTHER INFORMATION: → see error summary sheet item 11
 44 <400> SEQUENCE: 1
 45 gccagctagg atccgtcggg atgtcacac 29
 48 <210> SEQ ID NO: 2
 50 <211> LENGTH: 29
 52 <212> TYPE: DNA
 C--> 54 <213> ORGANISM: Artificial
 W--> 58 <220> FEATURE:
 W--> 58 <223> OTHER INFORMATION:
 58 <400> SEQUENCE: 2
 59 tcgatcgcgg ccgctcagta catgtccct 29
 62 <210> SEQ ID NO: 3
 64 <211> LENGTH: 29
 66 <212> TYPE: DNA
 C--> 68 <213> ORGANISM: Artificial
 W--> 72 <220> FEATURE:
 W--> 72 <223> OTHER INFORMATION: Some
 72 <400> SEQUENCE: 3
 73 gccagctagg atcccacaaa ctagtgcag 29
 76 <210> SEQ ID NO: 4
 78 <211> LENGTH: 37
 80 <212> TYPE: DNA
 C--> 82 <213> ORGANISM: Artificial
 W--> 86 <220> FEATURE:
 W--> 86 <223> OTHER INFORMATION: Some
 86 <400> SEQUENCE: 4
 87 tcgatcgaat tcccatggct ccagttgatc ttaaatac 37
 90 <210> SEQ ID NO: 5
 92 <211> LENGTH: 29
 94 <212> TYPE: DNA
 C--> 96 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/967,107

DATE: 11/06/2001

TIME: 09:43:10

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\11062001\I967107.raw

W--> 100 <220> FEATURE:

W--> 100 <223> OTHER INFORMATION:

same

100 <400> SEQUENCE: 5

101 gccagctagg atccctgggc atgtcacac

29

104 <210> SEQ ID NO: 6

106 <211> LENGTH: 29

108 <212> TYPE: DNA

C--> 110 <213> ORGANISM: Artificial

W--> 114 <220> FEATURE:

W--> 114 <223> OTHER INFORMATION:

same

114 <400> SEQUENCE: 6

115 tcgatcgcg cgccttagta catgtcctt

29

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/967,107

DATE: 11/06/2001

TIME: 09:43:11

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\11062001\I967107.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:44 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:54 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:58 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:68 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:72 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:72 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:82 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:86 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:86 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:96 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:100 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:100 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:110 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:114 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:114 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/967,107

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

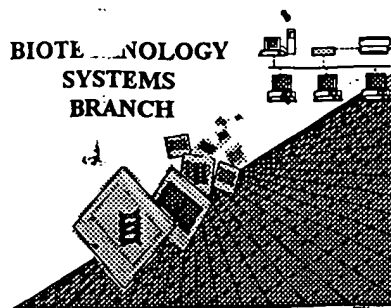
- 11 ✓ Use of <220> Sequence(s) plu missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

0590
10/19

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/967,107

Source: OPE

Date Processed by STIC: 11/6/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>